

# results of BLAST

### BLASTN 2.2.10 [Oct-19-2004]

#### Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1099000290-7310-211844646693.BLASTQ4

Query=

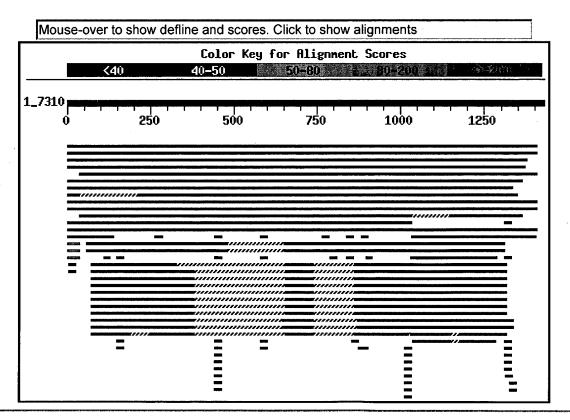
(1429 letters)

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
2,662,363 sequences; 12,059,721,380 total letters

If you have any problems or questions with the results of this search please refer to the  ${\tt BLAST\ FAQs}$ 

Taxonomy reports

## **Distribution of 122 Blast Hits on the Query Sequence**



Sequences producing significant alignments:	Score (bits)	E Value	
			GU
gi 46403042 ref NM 001571.2  Homo sapiens interferon regula	<u>2757</u>		GUE
gi 1107688 emb Z56281.1 HSIRF3MR H.sapiens mRNA for interfe	<u>2757</u>		
gi 50496727 emb CR615920.1  full-length cDNA clone CS0DC025	<u>2700</u>		U
gi 50493868 emb CR613061.1  full-length cDNA clone CS0DL002	<u> 2690</u>	0.0	U
gi 47940513 gb BC071721.1  Homo sapiens interferon regulato	<u> 2686</u>		GU
gi 50505771 emb CR624964.1  full-length cDNA clone CS0DL003	2672		U
gi 50477048 emb CR596241.1  full-length cDNA clone CS0DJ012	<u> 2611</u>		U
gi 50488926 emb CR608119.1  full-length cDNA clone CS0DI058	2252	0.0	
<pre>gi 33874467 gb BC009395.2  Homo sapiens interferon regulato</pre>	2010		GUE
gi 33875713 gb BC000660.2  Homo sapiens interferon regulato	2010		GU
gi 50471704 emb CR590897.1  full-length cDNA clone CS0DF028	<u>1939</u>		U
<u>gi 16553325 dbj AK057577.1 </u> Homo sapiens cDNA FLJ33015 fis, <u>gi 21747443 gb AC011495.8 </u> Homo sapiens chromosome 19 clone	$\frac{1931}{759}$	0.0	GU
gi 50494747 emb CR613940.1  full-length cDNA clone CS0CAP00	<u>745</u>		Ш
gi 47523299 ref NM 213770.1  Sus scrofa interferon regulato	529	e-147	
<pre>gi 40363626 dbj AB116563.1  Sus scrofa irf3 mRNA for interf</pre>	<u>529</u>	e-147	
gi 2149470 gb U86636.1 HSU86636 Homo sapiens interferon reg	283	6e-73	
gi 51895979 gb BC082274.1  Mus musculus interferon regulato	<u> 262</u>	2e-66	
gi 14707709 gb BC003233.1  Mus musculus interferon regulato	262	2e-66	
gi 23958540 gb BC023244.1  Mus musculus interferon regulato	<u>254</u>	5e-64	
gi 31980862 ref NM_016849.2  Mus musculùs interferon regula	<u>254</u>		G U.E
<pre>gi 29747995 gb BC050882.1  Mus musculus interferon regulato</pre>	<u>254</u>	5e-64	
gi 1658534 gb U75840.1 MMU75840 Mus musculus interferon reg	<u>254</u>	5e-64	
gi 1658532 gb U75839.1 MMU75839 Mus musculus interferon reg	<u>254</u>		GUE
<pre>gi 12851521 dbj AK013944.1  Mus musculus 13 days embryo hea</pre>	254		GUE
gi 53733560 gb BC083776.1  Rattus norvegicus interferon reg	<u>230</u>	7e-57	
gi 34856054 ref XM 214921.2  Rattus norvegicus similar to i	230	7e-57	
gi 4160492 gb AF112181.1 AF112181 Homo sapiens interferon r gi 29469629 gb AC126256.4  Mus musculus BAC clone RP24-235B	$\frac{170}{117}$	6e-39 7e-23	
gi 2674204 gb AF036341.1 AF036341 Mus musculus interferon r	86	3e-13	GE
gi 20336331 ref NM 052842.2  Homo sapiens BCL2-like 12 (pro	78		GUE
gi 20336329 ref NM 138639.1  Homo sapiens BCL2-like 12 (pro	<del>78</del>	6e-11	
gi 11093910 gb AF289220.1 AF289220 Homo sapiens Bcl-2 relat	<del></del> 78	6e-11	GΕ
qi 21263337 qb AC068522.7  Homo sapiens chromosome 8, clone	46	0.23	1.35
gi 20340506 gb AC009927.10  Homo sapiens chromosome 8, clon	46	0.23	
qi 19310327 gb AC106862.3        Homo sapiens BAC clone RP11-61L2         qi 18464299 gb AC099548.6        Homo sapiens BAC clone RP11-307I	$\frac{44}{44}$	0.89 0.89	
<u>qi 13443255 gb AC073264.5 </u> Homo sapiens BAC clone RP11-298A	44	0.89	
<u>qi 33875634 gb BC000609.2 </u> Homo sapiens KIAA0738 gene produ	44		GUE
gi 7662275 ref NM_014719.1  Homo sapiens KIAA0738 gene prod	44		GWE
<pre>gi 45382446 ref NM_205372.1  Gallus gallus interferon regul</pre>	44		GU
gi 7023017 dbj AK001640.1  Homo sapiens cDNA FLJ10778 fis,	44		GUE
<pre>gi 3882196 dbj AB018281.1  Homo sapiens mRNA for KIAA0738 p gi 52313394 emb BX890575.23  Zebrafish DNA sequence from cl</pre>	44	0.89 0.89	GWE

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G
                                                                         0.89
qi|14279398|qb|AF268079.1|AF268079 Gallus gallus interferon...
                                                                    44
                                                                               GΨ
                                                                         0.89
gi|790580|gb|U20338.1|GGU20338 Gallus gallus interferon reg...
                                                                    44
                                                                               GU
                                                                         3.5
gi|32330111|gb|AY251056.1|
                            Mus musculus EFEMP1 (Efemp1) mRN...
                                                                    42
                                                                               GU
                                                                         3.5
qi|37731916|qb|AY185605.1| Mus musculus EGF containing fibu...
                                                                    42
                                                                               G
                                                                    42
                                                                         3.5
qi|34879641|ref|XM 344273.1| Rattus norvegicus similar to E...
                                                                               GU
                              Rattus norvegicus similar to E...
                                                                    42
                                                                         3.5
qi|34879607|ref|XM 223725.2|
                                                                    42
gi|34102458|gb|AE016914.1| Chromobacterium violaceum ATCC 1...
                                                                         3.5
                                                                    42
gi|28476511|gb|AE016852.1|
                            Tropheryma whipplei str. Twist, ...
                                                                         3.5
                                                                               GUE
gi|22122482|ref|NM 146015.1|
                              Mus musculus epidermal growth ...
                                                                    42
                                                                         3.5
                                                                               GU
                                                                    42
qi|45827743|ref|NM 025074.3| Homo sapiens Fraser syndrome 1...
                                                                         3.5
                                                                               HO)
                                                                    42
                                                                         3.5
gi | 50926069 | gb | BC079455.1 |
                            Rattus norvegicus cDNA clone MGC...
gi|23266357|gb|AC013791.9|
                            Homo sapiens chromosome 11, clon...
                                                                    42
                                                                         3.5
                                                                               GU
gi|21410468|gb|BC031184.1|
                            Mus musculus epidermal growth fa...
                                                                    42
                                                                         3.5
                                                                               GŪ
qi|34367108|emb|BX647949.1|HSM808095 Homo sapiens mRNA; cDN...
                                                                    42
                                                                         3.5
                                                                               M
                                                                    42
                                                                         3.5
qi|34366577|emb|BX647420.1|HSM807565 Homo sapiens mRNA; cDN...
                                                                    42
qi|20279517|gb|AC104808.4| Homo sapiens BAC clone RP11-636J...
                                                                         3.5
gi|15876774|emb|AJ332356.1|HSA332356 Homo sapiens genomic s...
                                                                    42
qi|23306225|emb|AL928742.3|CNS08CBF Human chromosome 14 DNA...
                                                                    42
                                                                         3.5
                                                                    42
                                                                         3.5
qi|28191473|gb|AC104564.11|
                             Homo sapiens chromosome 17, clo...
                                                                               M
                                                                    42
                                                                         3.5
gi|50949879|emb|CR627393.1| Homo sapiens mRNA; cDNA DKFZp68...
                                                                               GUE
                                                                    42
                                                                         3.5
qi|29421197|dbj|AB040933.2|
                             Homo sapiens mRNA for KIAA1500 ...
gi | 6715703 | gb | AC007225.2 | AC007225 Homo sapiens chromosome 1...
                                                                    42
                                                                         3.5
                                                                    42
gi|15451494|gb|AC007419.7| Drosophila melanogaster, chromos...
                                                                         3.5
                                                                               GU
                                                                    42
qi|21734227|emb|AL833581.1|HSM804894 Homo sapiens mRNA; cDN...
                                                                         3.5
                                                                               G
qi|29420379|emb|AJ512501.1|HSA512501 Homo sapiens FRAS1 qen...
                                                                    42
                                                                         3.5
                                                                               42
                                                                         3.5
qi|3850601|qb|AC005950.1|AC005950 Homo sapiens Chromosome 1...
qi|14578120|qb|AC092239.1|AC092239 Drosophila melanoqaster,...
                                                                    42
                                                                         3.5
qi|22945691|qb|AE003611.3| Drosophila melanoqaster chromoso...
                                                                    42
gi|3347820|gb|AC005333.1|AC005333 Drosophila melanogaster D...
                                                                    42
                                                                         3.5
gi|21436704|emb|AL611984.15| Mouse DNA sequence from clone ...
                                                                    42
                                                                         3.5
qi|24743313|emb|AL662876.23| Mouse DNA sequence from clone ...
                                                                    42
qi|27115949|emb|AL954346.7| Mouse DNA sequence from clone R...
                                                                    42
                                                                         3.5
                                                                               GU
                                                                    42
gi|26346173|dbj|AK077302.1|
                             Mus musculus adult male xiphoid...
                                                                         3.5
gi|37674341|gb|AC115741.9| Mus musculus chromosome 14, clon...
                                                                    42
                                                                         3.5
                                                                               W
gi|26088730|dbj|AK041921.1| Mus musculus 3 days neonate thy...
                                                                   42
                                                                         3.5
                                                                               gi|2429082|dbj|D89730.1| Rattus rattus T16 mRNA, complete cds
                                                                   42
                                                                         3.5
```

#### Alignments

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Get selected sequences

Select all

Deselect all

| Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all | Deselect all |
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Query: 1 ggttccagctgcccgcacqccccqaccttccatcqtaqqccqqaccatqqqaaccccaaa 60

Sbjct:	201		260
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Sbjct:	261	gccacggatcctgccctggctggtgtcgcagctggacctggggcaactggagggcgt	317
Query:	121	ggcctgggtgaacaagagccgcacgcgcttccgcatcccttggaagcacggcctacggca	180
Sbjct:	318	ggcctgggtgaacaagagccgcacgcgcttccgcatcccttggaagcacggcctacggca	377
Query:	181	ggatgcacagcaggaggatttcggaatcttccaggcctgggccgaggccactggtgcata	240
Sbjct:	378	ggatgcacagcaggaggatttcggaatcttccaggcctgggccgaggccactggtgcata	437
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Query:	301	caaccgcaaagaagggttgcgtttagcagaggaccggagcaaggaccctcacgacccaca	360
Sbjct:		caaccgcaaagaagggttgcgtttagcagaggaccggagcaaggaccctcacgacccaca	557
Query:	361	taaaatctacgagtttgtgaactcaggagttggggacttttcccagccag	420
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Sbjct:	918		977
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Sbjct:	1038	gctgagctgcctgggtggggactggctctctggcgggccgggcagtggctctgggccca	1097
Query:	901	gcggctggggcactgccacacatactgggcagtgagcgaggagctgctccccaacagcgg	960
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Query:	961	gcatgggcctgatggcgaggtccccaaggacaaggaagga	1020
Sbjct:	1158	$\tt gcatgggcctgatggcgaggtccccaaggacaaggaagga$	1217
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Sbjct:	1218	$\verb cttcattgtagatctgattaccttcacggaaggaagcggacgctcaccacgctatgccct \\$	1277
Query:	1081	ctggttctgtgtgggggagtcatggcccaggaccagccgtggaccaagaggctcgtgat	1140
Sbjct:	1278	$\verb ctggttctgtgtgggggagtcatggcccaggaccagccgtggaccaagaggctcgtgat \\$	1337
		ggtcaaggttgtgcccacgtgcctcagggccttggtagaaatggcccgggtagggggtgc	
Sbjct:	1338	ggtcaaggttgtgcccacgtgcctcagggccttggtagaaatggcccgggtaggggtgc	1397
_		ctcctccctggagaatactgtggacctgcacatttccaacagccacccac	
Sbjct:	1398	ctcctccctggagaatactgtggacctgcacatttccaacagccacccac	1457
		ctccgaccagtacaaggcctacctgcaggacttggtggagggcatggatttccagggccc	
Sbjct:	1458	$\verb ctccgaccagtacaaggcctacctgcaggacttggtggagggcatggatttccagggccc \\$	1517
		tggggagagetgagecetegeteeteatggtgtgeeteeaacececetgtteeceaecae	
Sbjct:	1518	tggggagagctgagcctcgctcctcatggtgtgcctccaaccccctgttcccaccac	1577
1		ctcaaccaataaactggttcctgctatg 1408	
sbjct:	1578	ctcaaccaataaactggttcctgctatg 1605	

```
GUE H.sapiens mRNA for interferon regulatory
__>gi|1107688|emb|Z56281.1|HSIRF3MR
      Length = 1407
Score = 2757 bits (1391), Expect = 0.0
Identities = 1404/1408 (99%), Gaps = 3/1408 (0%)
Strand = Plus / Plus
       qqttccaqctqcccqcacqccccqaccttccatcgtaggccggaccatgggaaccccaaa 60
Query: 1
        ggttccagctgcccgcacgcccttccatcgtaggccggaccatgggaaccccaaa 60
Sbjct: 1
       gccacggntcctgcctggctggtgtcgcagctggacctggggnaacaactggagggcgt 120
Query: 61
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Sbjct: 61
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Sbjct: 118
Query: 181 ggatgcacagcaggaggatttcggaatcttccaggcctgggccgaggccactggtgcata 240
        ggatgcacagcaggaggatttcggaatcttccaggcctgggccgaggccactggtgcata 237
Sbjct: 178
Query: 241 tgttcccgggagggataagccagacctgccaacctggaagaggaatttccgctctgccct 300
        Sbjct: 238 tgttcccgggagggataagccagacctgccaacctggaagaggaatttccgctctgccct 297
Query: 301
       caaccgcaaagaagggttgcgtttagcagaggaccggagcaaggaccctcacgacccaca 360
        caaccqcaaagaagggttqcgtttagcagaggaccggagcaaggaccctcacgacccaca 357
Sbjct: 298
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Query: 421
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Sbjct: 478
Query: 541
       tgagccctgccctcagcccctgcgqagccccagcttggacaatcccactcccttcccaaa 600
        Sbjct: 538 tgagecetgecetcageceetgeggageeceagettggacaateceaeteeetteecaaa 597
Query: 601
       cctggggccctctgagaacccactgaagcggctgttggtgccgggggaagagtgggaqtt 660
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Sbjct:	598	cctggggccctctgagaacccactgaagcggctgttggtgccgggggaagagtgggagtt	657
Query: Sbjct:		cgaggtgacagccttctaccggggccgccaagtcttccagcagaccatctcctgcccgga	720 717
Query: Sbjct:		gggcctgcggctggtggggtccgaagtgggagacaggacgctgcctggatggccagtcac	780 777
Query: Sbjct:		actgccagaccctggcatgtccctgacagacaggggagtgatgagctacgtgaggcatgt	840 837
Query: Sbjct:		gctgagctgcctgggtgggggactggctctctggcgggccgggcagtggctctgggccca	900 897
Query: Sbjct:		gcggctggggcactgccacacatactgggcagtgagcgaggagctgctccccaacagcgg	960 957
Query: Sbjct:		gcatgggcctgatggcgaggtccccaaggacaaggaagga	1020 1017
		cttcattgtagatctgattaccttcacggaaggaagcggacgctcaccacgctatgccct	1080 1077
		ctggttctgtgtggggagtcatggccccaggaccagccgtggaccaagaggctcgtgat	
		ggtcaaggttgtgcccacgtgcctcagggccttggtagaaatggcccgggtagggggtgc	
		ctcctccctggagaatactgtggacctgcacatttccaacagccacccac	
		ctccgaccagtacaaggcctacctgcaggacttggtggagggcatggatttccagggccc	
Query:	1321	tggggagagetgagecetegeteeteatggtgtgeeteeaacececetgtteeecaceac	1380

```
Sbjct: 1318 tggggagagetgagecetegeteeteatggtgtgeeteeaacececetgtteeecaceae 1377
Query: 1381 ctcaaccaataaactggttcctgctatg 1408
        Sbjct: 1378 ctcaaccaataaactggttcctgctatg 1405
□>gi|50496727|emb|CR615920.1|  ull-length cDNA clone CS0DC025YB10 of Neuroblast
        25-normalized of Homo sapiens (human)
       Length = 1547
Score = 2700 \text{ bits } (1362), \text{ Expect = } 0.0
Identities = 1375/1379 (99%), Gaps = 3/1379 (0%)
Strand = Plus / Plus
        ggttccagctgcccgcacgcccgaccttccatcgtaggccggaccatgggaaccccaaa 60
Query: 1
        Sbjct: 172
        ggttccagctgcccgcacgccccgaccttccatcgtaggccggaccatgggaaccccaaa 231
Query: 61
        gccacggntcctgccctggctggtgtcgcagctggacctggggnaacaactggaggcgt 120
        Sbjct: 232
        gccacggatcctgccctggctggtgtcgcagctggacctgggg---caactggaggcgt 288
Query: 121
        ggcctgggtgaacaagagccgcacgcgcttccgcatcccttggaagcacggcctacggca 180
        Sbjct: 289
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Query: 181
        ggatgcacagcaggaggatttcggaatcttccaggcctgggccgaggccactggtgcata 240
        Sbjct: 349
        ggatgcacagcaggaggatttcggaatcttccaggcctgggccgaggccactggtgcata 408
Query: 241
        tgttcccgggagggataagccagacctgccaacctggaagaggaatttccgctctgccct 300
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Sbjct: 409
Query: 301
        caaccgcaaagaagggttgcgtttagcagaggaccggagcaaggaccctcacgacccaca 360
        Sbjct: 469
        caaccgcaaagaagggttgcgtttagcagaggaccggagcaaggaccctcacgacccaca 528
Query: 361
        Sbjct: 529
        Query: 421
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